# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 21:49:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524302.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524302.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 21:49:10 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524302.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 656,563 |
| Mapped reads | 578,860 / 88.17% |
| Unmapped reads | 77,703 / 11.83% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,847 / 0.74% |
| Read min/max/mean length | 30 / 76 / 76.25 |
| Duplicated reads (estimated) | 10,957 / 1.67% |
| Duplication rate | 1.11% |
| Clipped reads | 582,365 / 88.7% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,701,100 / 23.28% |
| Number/percentage of C's | 6,244,988 / 18.88% |
| Number/percentage of T's | 10,570,944 / 31.96% |
| Number/percentage of G's | 8,553,287 / 25.86% |
| Number/percentage of N's | 4,682 / 0.01% |
| GC Percentage | 44.74% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0107 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1499 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.76 |

## 2.5. Mismatches and indels

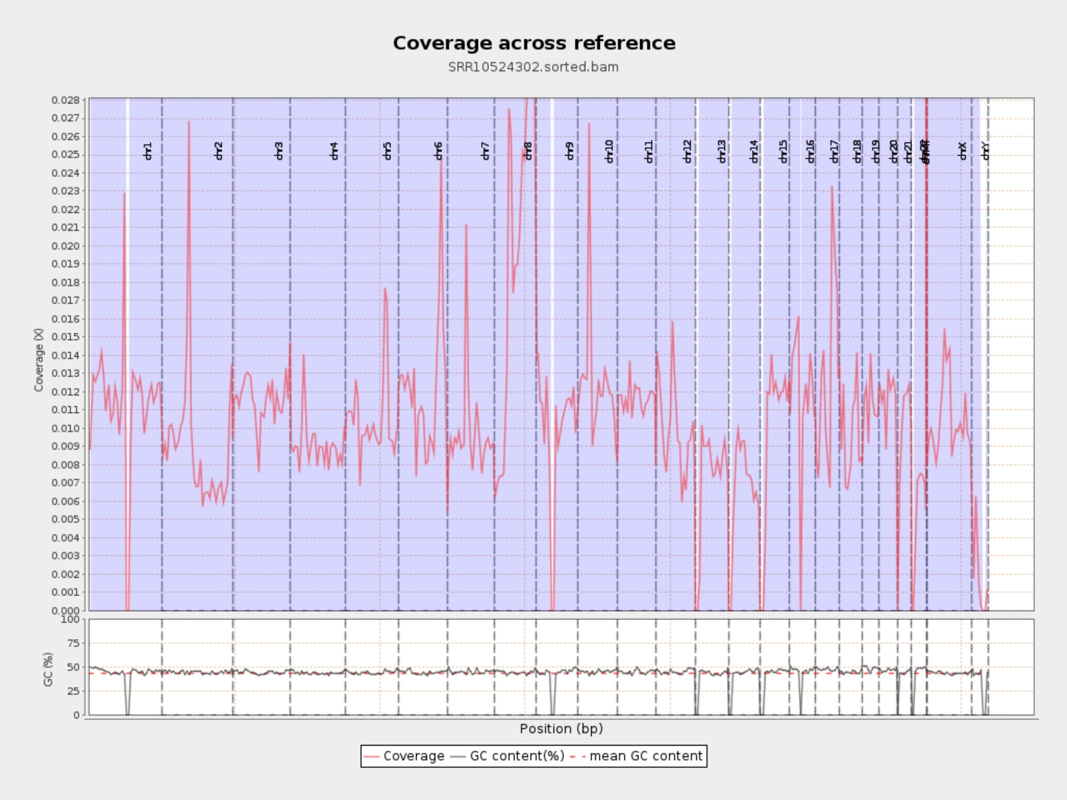
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 168,778 |
| Insertions | 2,267 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 4,808 |
| Mapped reads with at least one deletion | 0.83% |
| Homopolymer indels | 40.48% |

## 2.6. Chromosome stats

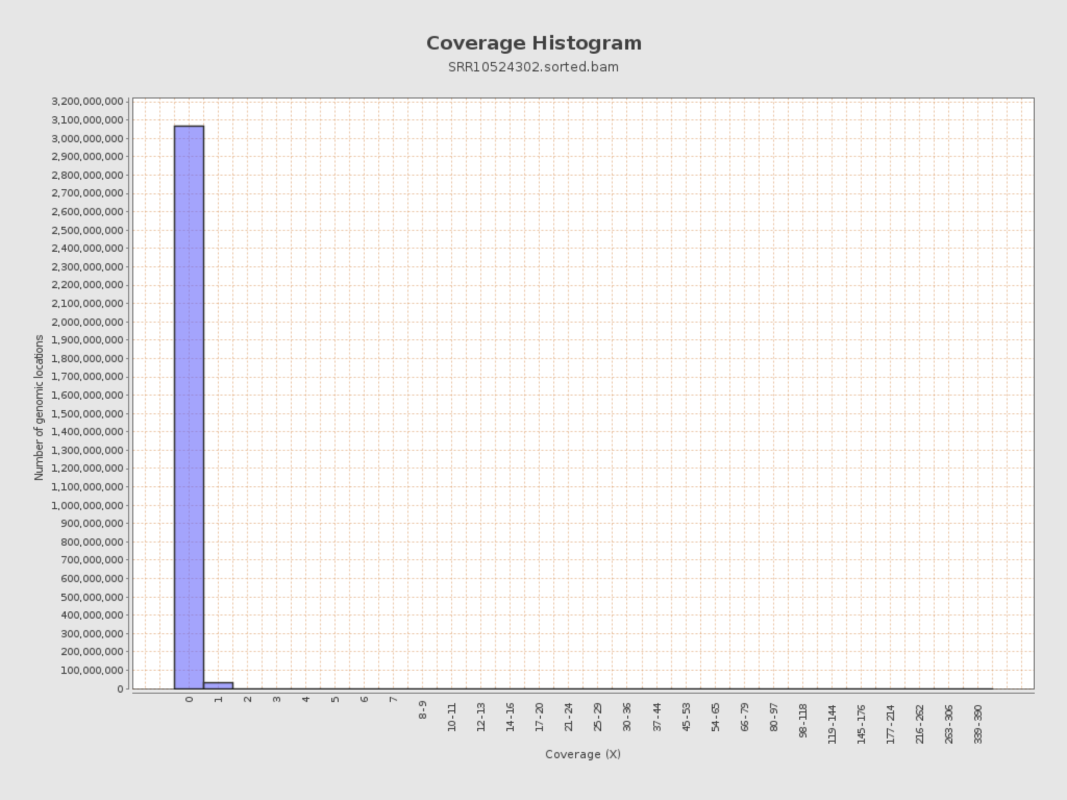
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2838731 | 0.0114 | 0.2845 |
| chr2 | 243199373 | 2189037 | 0.009 | 0.1619 |
| chr3 | 198022430 | 2280765 | 0.0115 | 0.1113 |
| chr4 | 191154276 | 1728372 | 0.009 | 0.1024 |
| chr5 | 180915260 | 1917774 | 0.0106 | 0.1065 |
| chr6 | 171115067 | 2070298 | 0.0121 | 0.1176 |
| chr7 | 159138663 | 1565553 | 0.0098 | 0.1835 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3227266 | 0.022 | 0.178 |
| chr9 | 141213431 | 1373913 | 0.0097 | 0.1209 |
| chr10 | 135534747 | 1699972 | 0.0125 | 0.1632 |
| chr11 | 135006516 | 1563306 | 0.0116 | 0.1282 |
| chr12 | 133851895 | 1337815 | 0.01 | 0.1038 |
| chr13 | 115169878 | 818928 | 0.0071 | 0.0866 |
| chr14 | 107349540 | 711251 | 0.0066 | 0.0903 |
| chr15 | 102531392 | 1011184 | 0.0099 | 0.1047 |
| chr16 | 90354753 | 1074688 | 0.0119 | 0.121 |
| chr17 | 81195210 | 1038474 | 0.0128 | 0.1224 |
| chr18 | 78077248 | 767975 | 0.0098 | 0.193 |
| chr19 | 59128983 | 669546 | 0.0113 | 0.2028 |
| chr20 | 63025520 | 732425 | 0.0116 | 0.1117 |
| chr21 | 48129895 | 459856 | 0.0096 | 0.1049 |
| chr22 | 51304566 | 261638 | 0.0051 | 0.0731 |
| chrMT | 16571 | 13573 | 0.8191 | 1.0238 |
| chrX | 155270560 | 1622578 | 0.0105 | 0.1183 |
| chrY | 59373566 | 107924 | 0.0018 | 0.061 |

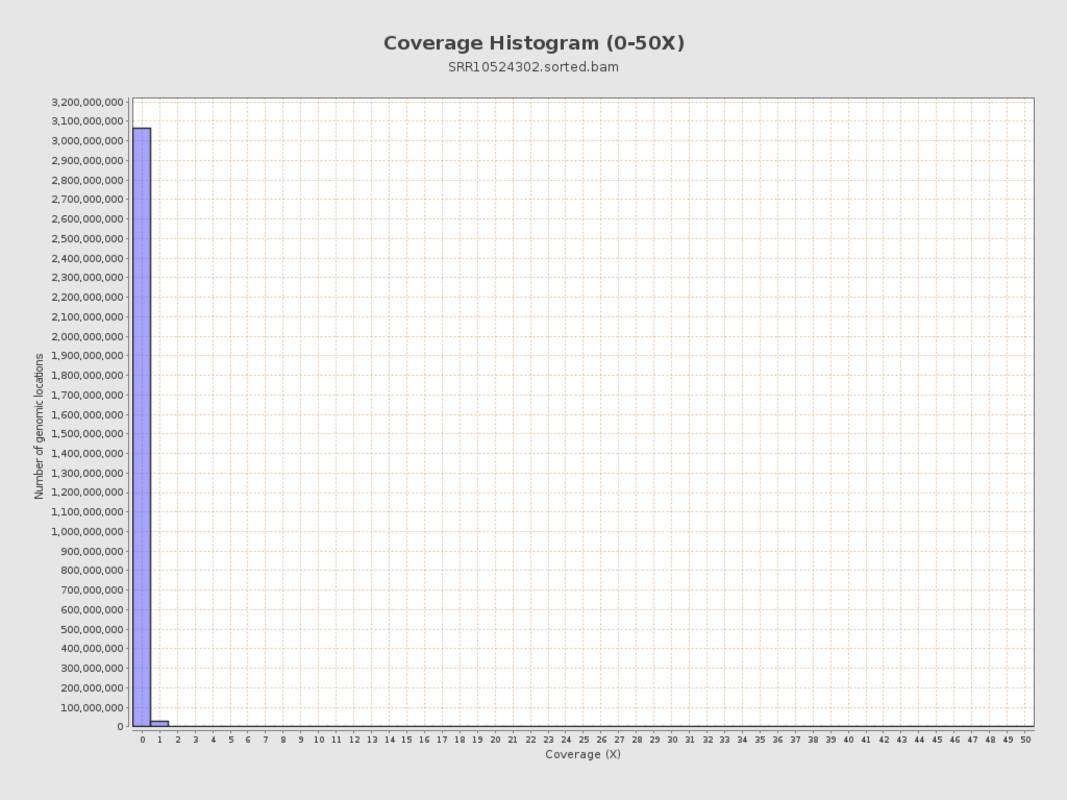
# 3. Results : Coverage across reference



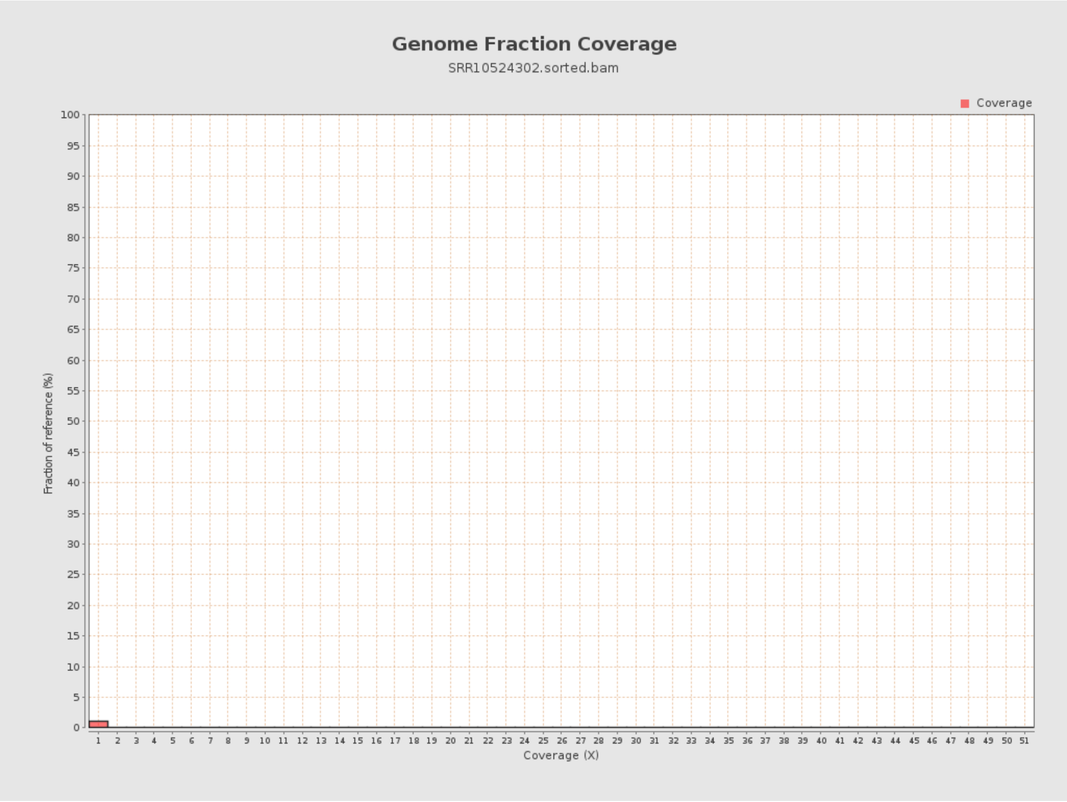
# 4. Results : Coverage Histogram



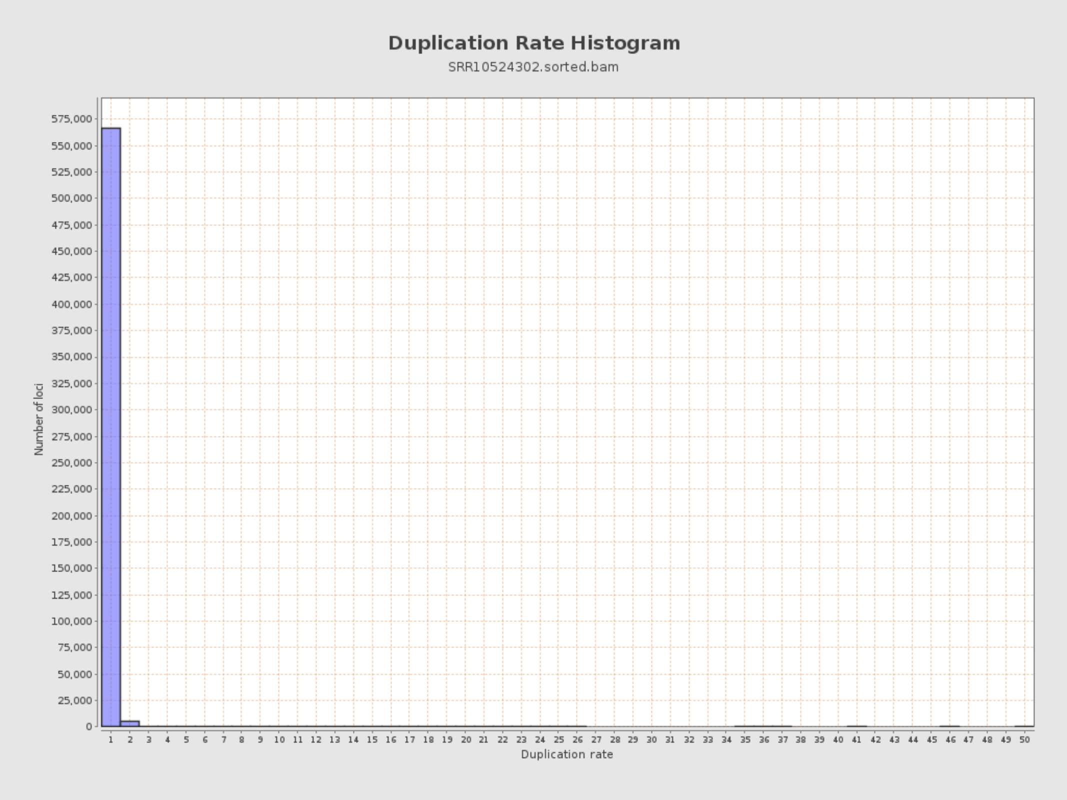
# 5. Results : Coverage Histogram (0-50X)



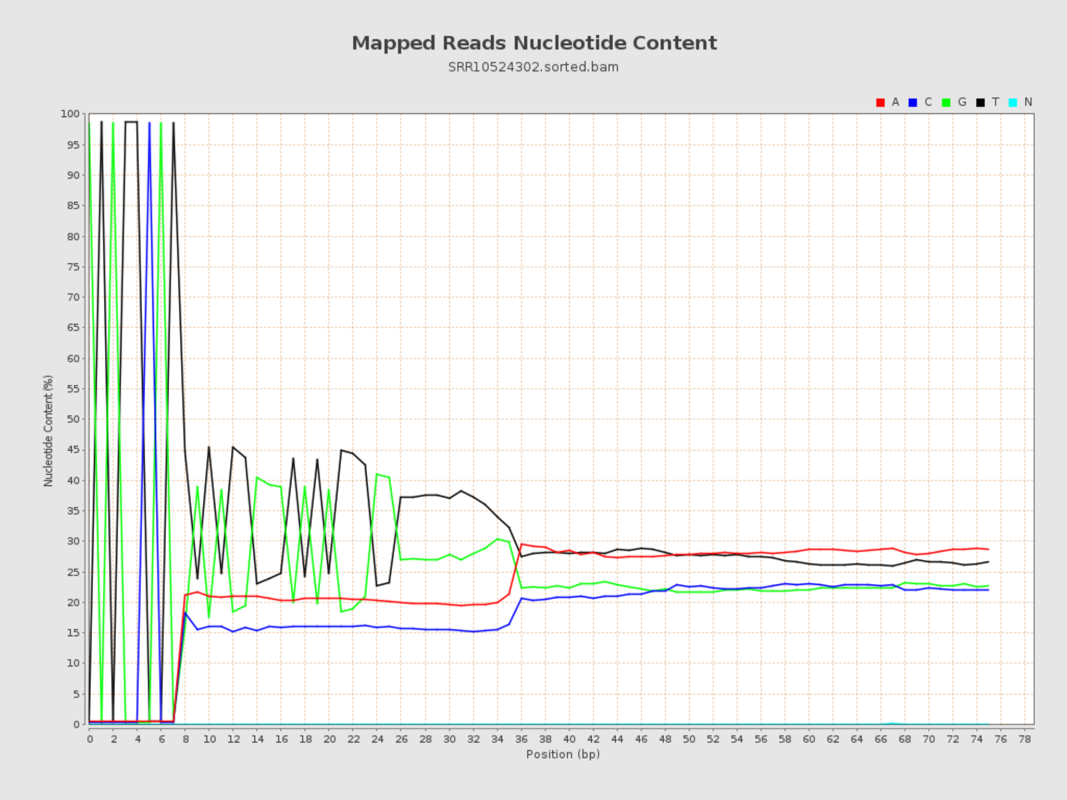
# 6. Results : Genome Fraction Coverage



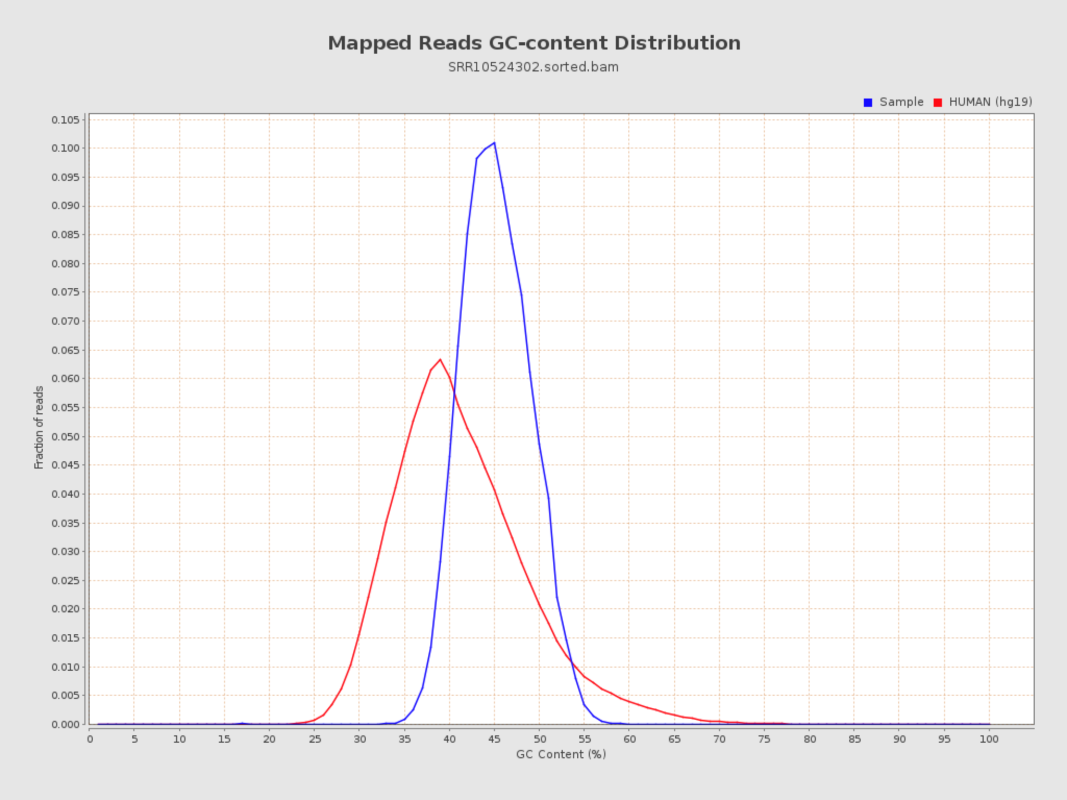
# 7. Results : Duplication Rate Histogram



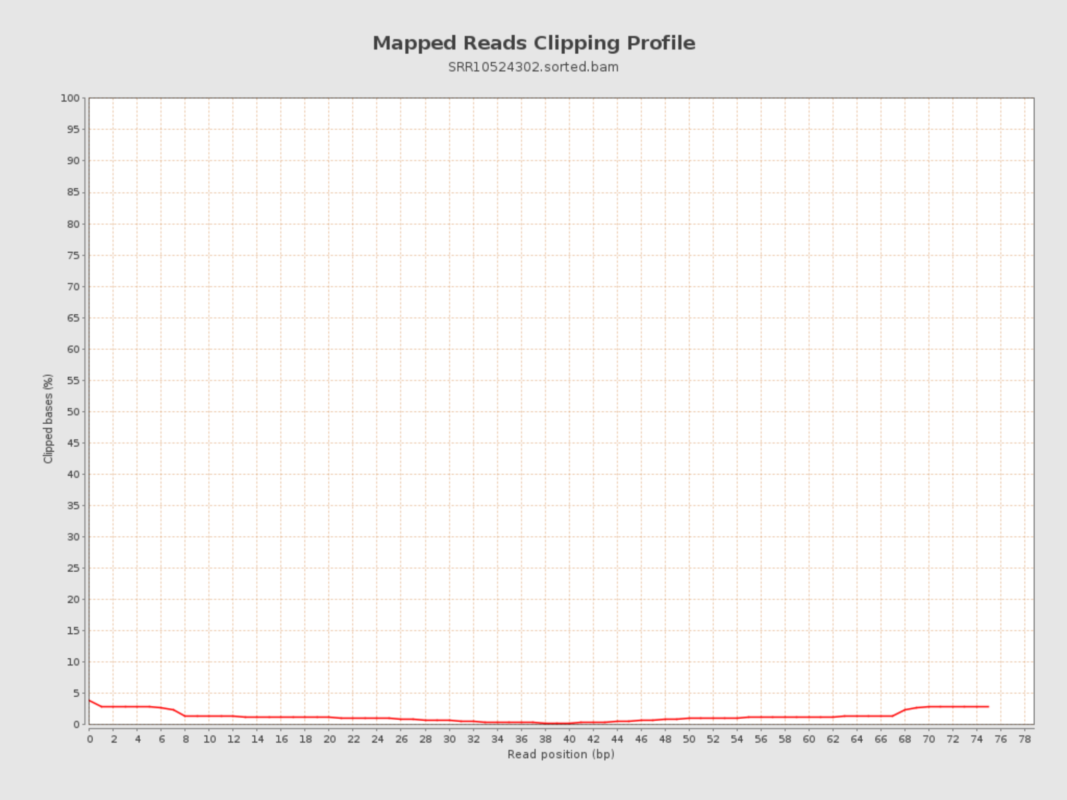
# 8. Results : Mapped Reads Nucleotide Content



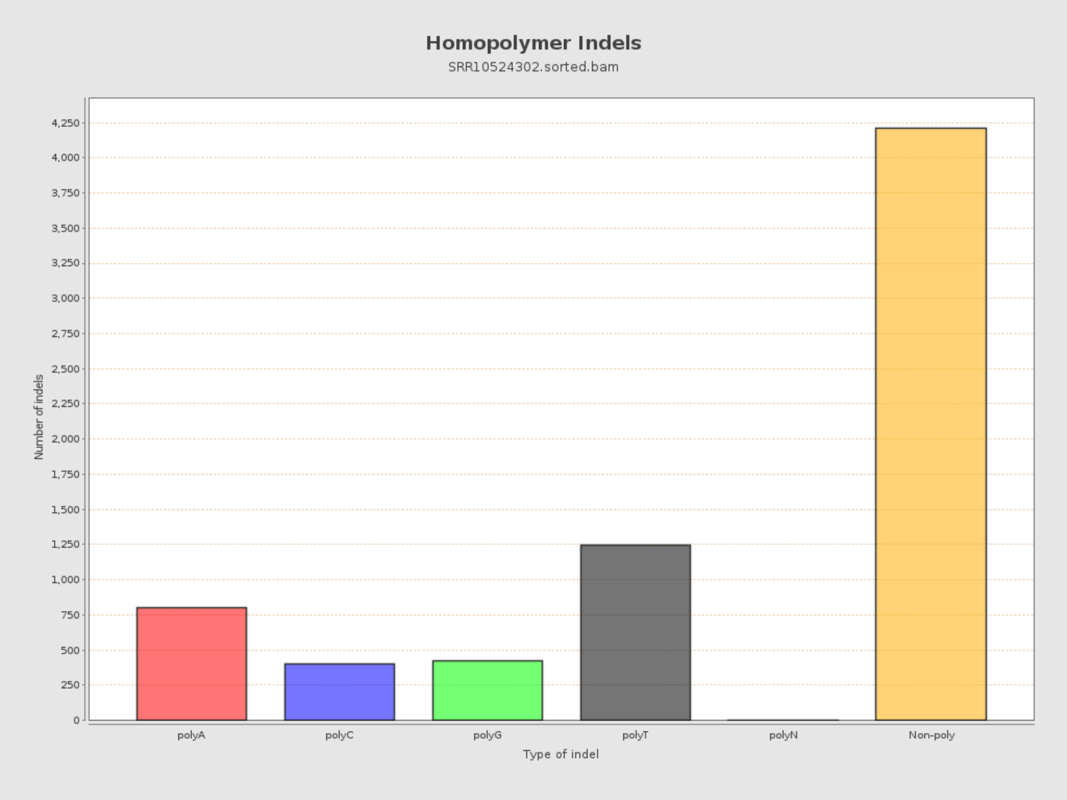
# 9. Results : Mapped Reads GC-content Distribution



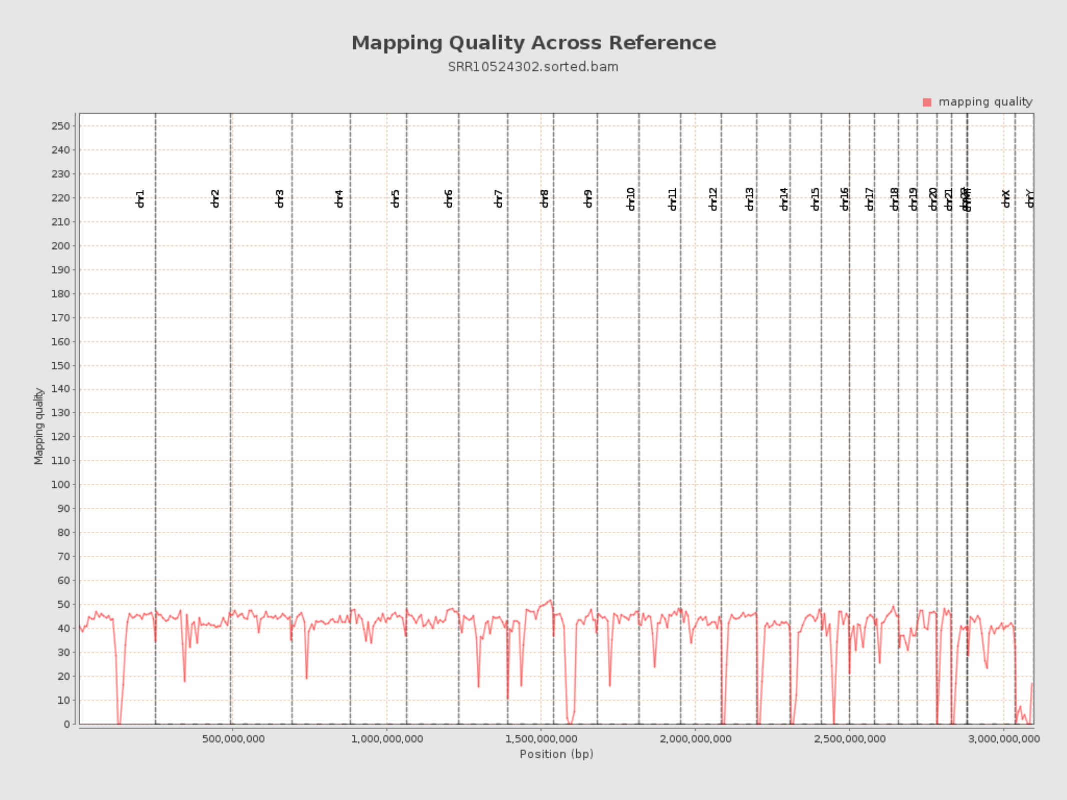
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram